

GenCore version 4.5
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Run on: March 1, 2001, 16:22:07 ; search time 88.16 Seconds
(without alignments)
26.590 Million cell updates/sec

Title:	OM protein - protein search, using sw model
Perfect score:	52
Scoring table:	US-09-331-631A-37
Sequence:	BLOSUM62DX
GapOp 10.0 , Gapext 0.5	
Searched:	374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters:	374700
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
	Maximum Match 100%
Database :	SPREMBL-15,*
	1: sp_archea;*
	2: sp_bacteria;*
	3: sp_fungi;*
	4: sp_human;*
	5: sp_invertebrate;*
	6: sp_mammal;*
	7: sp_mhc;*
	8: sp_organelle;*
	9: sp_phage;*
	10: sp_plant;*
	11: sp_rabbit;*
	12: sp_virus;*
	13: sp_vertebrate;*
	14: sp_unclassified;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	52	100	0	Q16861 homo sapien
2	52	100	0	Q9V18 drosophila
3	52	100	0	Q9RFB5 mycoplasma
4	52	100	0	P779377 sus scrofa
5	52	100	0	P779380 sus scrofa
6	52	100	0	Q23947 drosophila
7	52	100	0	Q23948 drosophila
8	52	100	0	Q9Y110 bungarus mu
9	52	100	0	Q9N9H2 ruditapes p
10	52	100	0	P82107 hirudo medi
11	52	100	0	Q9N9H1 ruditapes d
12	52	100	0	Q92044 cyprinodon
13	52	100	0	Q73014 notothenia
14	52	100	0	Q93593 chaenocepha
15	52	100	0	Q95609 trematomus
16	52	100	0	Q13259 chinonodraco
17	52	100	0	Q13258 chinonodraco
18	52	100	0	Q91b50 pagrus majus
19	52	100	0	Q91910 cyprinus ca

ALIGNMENTS

RESULT	1
ID	Q16861
AC	Q16861;
DT	01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT	01-AUG-1998 (TREMBLrel. 07, last annotation update)
DE	CYSTEINE-RICH PROTEIN (FRAGMENT).
OS	Homo sapiens (Human).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo;
OX	NCBI_TAXID=9606;
[1]	SEQUENCE FROM N.A.
RP	LeMasson I., Devaux C., Mesnard J.M.;
RA	Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RL	DR: U65332; NAB05810.1; -
DR	FT: NON_TER 1 1
FT	SO SEQUENCE 46 AA; 5061 MW; 311922FE40A4EBF CRC64;

SEQUENCE

Query	Match	Similarity	Best Local Similarity	Score	DB	Length	Indels	Gaps
			20.0%	52	4	46	0	0
Matches					4;	Conservative	Mismatches	
Qy	1	CXXXXCXXXXXXXXXXXXCXXC	20			16	0;	0;
Db	11	CCCCCCCCCC	30					

RESULT

2
Q9VIV8
ID Q9VIV8
AC Q9VIV8;
DT 01-MAY-2000 (TREMBLrel. 13, created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG17567 PRCTEIN.
GN CG17567.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydrioidea; Drosophilidae; Drosophila.
 OX NCBI_TAXID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=9731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson G.R., Miklos G.I.G.,
 RA Abril J.F., Agayamai A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bochkov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brostkin P., Brottier P.,
 RA Burts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Goforth A., Gong J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Tbegyan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechumian K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kraitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levintsky T.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.A., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Nelson S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puriv V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Staelton M., Strong R., Sun E.,
 RA Svistekas R., Tector C., Turner A.H., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Winstock G.M., Weissbach J.,
 RA Williams S. M., Woodrige T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000);
 DR EMBL; AE003662; AAFR373; 1; -
 DR FLIBASE; FBgn0040994; CG17567;
 DR SEQUENCE 47 AA; 4909 MW; 19478A884B06D652 CRC64;
 DR SQ

Query Match 100.0%; Score 52; DB 5; Length 47;
 Best Local Similarity 20.0%; Pred. No. 79;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXCXXXXC 20

RESULT 4

ID P79377 PRELIMINARY; PRT; 48 AA.

P79377 AC 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE METALLOTHIONEIN (MT) (FRAGMENT).
 OS Sus scrofa (PIG).

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TAXID=9823; [1]
 RN SEQUENCE FROM N.A.

RC TISSUE=LIVER;
 RX MEDLINE=9911554; PubMed=9916088;
 RA Huang M.C., Pan P.K., Zeng T.-F., Chen N.C., Peng J.Y., Huang P.C.,
 RA "Multiple isoforms of metallothionein are expressed in the porcine
 liver.;"
 RL Gene 211:49-55(1998);
 CC !- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 CC TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 CC GLUCOCORTICOIDS.
 DR EMBL; AB00789; BA019179.1; -
 DR HSSP; P02795; IMHU
 DR INTERPRO; IPR000006; -
 DR INTERPRO; IPR003019; -
 DR PFAM; PF00131; metathio; 1.
 DR PRINTS; PRO0860; MTWTERTRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 DR Metal-binding; Metal-thiolate cluster; Chelation; Zinc.
 FT NON_TER 48 48
 FT METAL 24 24 CLUSTER.
 FT METAL 27 27 CLUSTER.
 FT METAL 17 17 CLUSTER.
 FT METAL 19 19 CLUSTER.
 FT METAL 22 22 CLUSTER.
 FT METAL 31 31 CLUSTER.
 SQ SEQUENCE 48 AA; 4704 MW; FOF5AC96BB9EBD19 CRC64;

Query Match 100.0%; Score 52; DB 6; Length 48;
 Best Local Similarity 20.0%; Pred. No. 80;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXCXXXXC 21

RESULT 3

ID Q9RFPS PRELIMINARY; PRT; 48 AA.

Q9RFPS ID Q9RFPS; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DB 01-MAY-2000 (TREMBLrel. 13, last annotation update)

DE ORFE2; Mycoplasma fermentans; Bacteria; Firmicutes; Bacillus/clostridium group; Mollicutes; Mycoplasmataceae; Mycoplasma. NCBI_TAXID=2115; [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=PG18;

QY	1 CXXCXXXXXXXCXXXC 20	RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
ID	!:::!:!:!:!:!:!:!:!:!:!	DR EMBL; X5811; CAR4117.1;
AC	P9380; PRELIMINARY; PRT; 48 AA.	DR FLIXBASE; FBgn0015096; DhydMst87Fa.
DT	01-MAY-1997 (TREMBLrel. 03, Created)	DR INTERPRO; IPR001450; -
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)	DR PROSITE; PS00198; 4FEBS_FERREDOXIN; UNKNOWN_1.
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	SQ SEQUENCE 49 AA; 4610 MW; BE158FED51369F01 CRC64;
DE	METALLOTHIONEIN (MT) (FRAGMENT).	
OS	Sus scrofa (Pig); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus.	
OC		
OC		
OX	NCBI_TaxID=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=LIVER;	
RX	MEDLINE:98241500; PubMed=9573337;	
RA	Huang M.C., Pan P.K., Zeng T.-F., Chen N.C., Peng J.Y., Huang P.C.;	
CC	"Multiple isoforms of metallothionein are expressed in the porcine liver."	
CC		
EMBL	AB00195; BA19184.1; -.	
DR		
DR	P02795; 2MIU;	
DR	INTERPRO; IPR00006; -.	
DR	PRINTS; PR00131; metathio; 1.	
DR	PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.	
KW	Metal-binding; Metal-thiolate cluster; Chelation; Zinc.	
FT	NON_TER 48	
FT	METAL 24	CLUSTER.
FT	METAL 27	CLUSTER.
FT	METAL 17	CLUSTER.
FT	METAL 19	CLUSTER.
FT	METAL 22	CLUSTER.
FT	METAL 31	CLUSTER.
SQ	SEQUENCE 48 AA; 4727 MW; 3BC2E2EB0686216 CRC64;	
Query Match 100.0%; Score 52; DB 6; Length 48; Best Local Similarity 20.0%; Pred. No. 80; Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CXXXCXXXXXXXCXXXC 20	
Db	29 CKKSCCCSCPAGCARCAOGC 48	
RESULT 6		
RESULT 6		
ID	Q33947; PRELIMINARY; PRT; 49 AA.	
AC	O23947; PRELIMINARY; PRT; 49 AA.	
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	TESTIS-SPECIFIC RNA.	
GN	Drosophila hydei (Fruit fly).	
OS	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Drosophilidae; Drosophila.	
OC		
OX	NCBI_TaxID=7224;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	Kuech A., Buenemann H.;	
RX	Submitted (DEC-1990) to the EMBL/GenBank/DDJB databases.	
RA	Drosophila hydei (Fruit fly).	
DR	Submitted (DEC-1990) to the EMBL/GenBank/DDJB databases.	
DR	EMBL; X58114; CA44118.1; -.	
DR	FLIXBASE; FBgn0015097; DhydMst87Fa.	
DR	INTERPRO; IPR001450; -.	
DR	PROSITE; PS00198; 4FEAS_FERREDOXIN; UNKNOWN_1.	
SQ	SEQUENCE 49 AA; 4550 MW; 24758FEC51369F1D CRC64;	
Query Match 100.0%; Score 52; DB 5; Length 49; Best Local Similarity 20.0%; Pred. No. 81; Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CXXCXXXXXXXCXXXC 20	
Db	23 CGGCPYCSCGRCYCSCGCC 42	
RESULT 8		
ID	Q9Y10; PRELIMINARY; PRT; 54 AA.	
AC	O9Y10; PRELIMINARY; PRT; 54 AA.	
DT	01-MAY-1999 (TREMBLrel. 10, Created)	
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	ALPHA-BUNGAROTOxin ISOFORM R7 (FRAGMENT).	
OS	Bungarus multicinctus (Many-banded Krait).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Bungarinae; Bungarus.	
OC		
OX	NCBI_TaxID=8616;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=VENOM GLAND;	
RX	MEDLINE:9905807; PubMed=9837992;	
RA	Liu L.F., Chang C.C., Lian M.Y., Kuo K.W.;	
RT	"Genetic characterization of the mRNAs encoding alpha-bungarotoxin isoforms and RNA editing in Bungarus multicinctus gland cells.";	
RL	Nucleic Acids Res. 26:5624-5629(1998).	
DR	EMBL; AF056407; AAC83988.1; -.	
RA	Kuech A., Buenemann H.;	

DR	HSSP-P01378; IABT.
INTERPRO	IPR000027; -.
PFAM	PF00087; toxin_1.
NON_TER	1
SEQUENCE	54 AA; 5783 MW; F30BB6043B62700 CRC64;
QY	1 CXXXGXXXXXXGXXXCC 20 ::: ::: ::: ::: ::: :::
DB	29 CDAPCSSKGKVVELGCAATC 48
RESULT	9
ID	Q9NH2
PRELIMINARY	
PRT	57 AA.
AC	Q9NH2;
DT	01-OCT-2000 (TREMBREL_15, Created)
DE	01-OCT-2000 (TREMBREL_15, Last sequence update)
DE	METALLOTHIONEIN (FRAGMENT).
MT	
RC	Ruditapes philippinarum.
OS	Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC	Veneroidea; Veneridae; Ruditapes.
OX	NCBI_TaxID=104384;
RN	[1]
SEQUENCE FROM N_A.	
TISSUE=GILL;	
RA	Moraga D., Tanguy A.;
RT	"Characterisation of metallothioneins sequences in three clams Rudittapes decussatus, Ruditapes philippinarum and venerupis pullastria.";
RT	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AJ249686; CAB96403.1; -.
FT	NON_TER 1
FT	NON_TER 57
FT	NON_TER 57
SQ	57 AA; 5411 MW; F7B37567623FD7DD CRC64;
Query Match	100.0%; Score 52; DB 5; Length 57;
Best Local Similarity	20.0%; Pred. No. 88;
Matches	4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY	1 CXXXGXXXXXXGXXXCC 20 ::: ::: ::: ::: ::: :::
DB	23 CGPGCKCGDKCGCKVKG 42
RESULT	10
ID	P82107
PRELIMINARY	
PRT	59 AA.
AC	P82107;
DT	01-MAY-2000 (TREMBREL_13, Created)
DT	01-MAY-2000 (TREMBREL_13, Last sequence update)
DT	01-OCT-2000 (TREMBREL_15, Last annotation update)
DE	BDELLASTASIN (BDELLIN_A).
OS	Hirudo medicinalis (Medicinal leech);
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Apynochordellida; Hirudiniformes; Hirudinidae; Hirudo;
OX	NBII_TaxID=6421;
RN	[1]
SEQUENCE	
RA	Moser M., Auerswald E., Mentele R., Eckerskorn C., Fritz H., Fink E.;
RT	"Bdellastatin, a serine protease inhibitor of the antistasins family from the medicinal leech (Hirudo medicinalis). Primary structure, expression in yeast, and characterization of native and recombinant inhibitor.";
RT	Eur J. Biochem. 253:212-220(1998).
RL	-1. FUNCTION: STRONG INHIBITOR OF MAMMALIAN TRYPSIN, PLASMIN AND CC
CC	-1. MASS SPECTROMETRY: MW=6332.6; METHOD=ELECTROSspray.
CC	-1. SIMILARITY: BELONGS TO THE ANTISTASIN FAMILY.
DR	HSSP; P80302; 1HA.
KW	Serine protease inhibitor.
FT	ACT SITE 34
DE	DISULFID 10
FT	DISULFID 15
FT	DISULFID 28
FT	DISULFID 33
FT	DISULFID 37
SQ	SEQUENCE 59 AA; 6343 MW; 43BA5BB2D0E403A9 CRC64;
Query Match	100.0%; Score 52; DB 5; Length 59;
Best Local Similarity	20.0%; Pred. No. 90;
Matches	4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY	1 CXXXGXXXXXXGXXXCC 20 ::: ::: ::: ::: ::: :::
DB	33 CKVKCEHGFKKDDNGCEVAC 52
RESULT	11
ID	Q9NHL
PRELIMINARY	
PRT	59 AA.
AC	Q9NHL;
DT	01-OCT-2000 (TREMBREL_15, Created)
DT	01-OCT-2000 (TREMBREL_15, Last sequence update)
DE	METALLOTHIONEIN (FRAGMENT).
GN	MT.
OS	Ruditapes decussatus.
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC	Veneroidea; Veneridae; Ruditapes.
OX	NCBI_TaxID=104385;
RN	[1]
SEQUENCE FROM N_A.	
RC	TISSUE=GILL;
RA	Moraga D., Tanguy A.;
RT	"Characterisation of metallothioneins sequences in three clams pullastria.";
RT	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AJ249687; CAB96402.1; -.
FT	NON_TER 1
FT	NON_TER 59
SQ	SEQUENCE 59 AA; 5613 MW; CAB87C9FE35EC8A2 CRC64;
Query Match	100.0%; Score 52; DB 5; Length 59;
Best Local Similarity	20.0%; Pred. No. 90;
Matches	4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
QY	1 CXXXGXXXXXXGXXXCC 20 ::: ::: ::: ::: ::: :::
DB	10 CWCSCSDCPATGCKCGPGC 29
RESULT	12
ID	Q2044
PRELIMINARY	
PRT	60 AA.
AC	Q2044;
DT	01-NOV-1996 (TREMBREL_01, Created)
DT	01-NOV-1996 (TREMBREL_01, Last sequence update)
DT	01-OCT-2000 (TREMBREL_15, Last annotation update)
DE	METALLOTHIONEIN (MT).
GN	MT_A.
OS	Cyprinodon sp.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Athinemorpha; Cyprinodontiformes; Cyprinodontidae; Cyprinodon.

OX NCBI_TaxID=48417;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Kille P., Olsson P.E.; to the EMBL/GenBank/DDBJ databases.
 RL Submitted (APR-1996) -!
 CC FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 GLUCOCORTICOIDS.
 EMBL; X97273; CAA65928.1; -.
 HSP; P02802; IDFS.
 DR INTERPRO; IPR000006; -.
 DR INTERPRO; IPR003019; -.
 PRAM; PF00131; metallothio; 1.
 PRINTS; PR00860; MTVERTEBRATE.
 PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 DR Metal-binding; Metal-thiolate cluster; Chelation; zinc.
 KW METAL-binding; metal-thiolate cluster; chelation; zinc.
 FT METAL 23 23 CLUSTER.
 FT METAL 26 26 CLUSTER.
 FT METAL 16 16 CLUSTER.
 FT METAL 18 18 CLUSTER.
 FT METAL 21 21 CLUSTER.
 SQ SEQUENCE 60 AA; 6019 MN; E866E715A2C424A CRC64;

Query Match 100.0%; Score 52; DB 13; Length 60;
 Best Local Similarity 20.0%; Pred. No. 91;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXXXCXXXXXXCXXXC 20
 Db 28 CKKSCCPCCPSGCKASGC 47

RESULT 13
 ID 073914 PRELIMINARY; PRT; 60 AA.
 AC 073914;
 DR 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE METALLOTHIONEIN (MT).
 MT.
 GN Chaenocephalus aceratus.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;
 OC Nototenioidae; Channichthyidae; Chaenocephalus;
 OX NCBI_TaxID=36190;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Carginale V., Capasso C., Scudiero R., Parisi E.;
 CC "Metallothionein in Antarctic organisms.";
 DR Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 GLUCOCORTICOIDS.
 DR PRINTS; PR00860; MTVERTEBRATE.
 PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 DR Metal-binding; Metal-thiolate cluster; Chelation; zinc.
 FT METAL 23 23 CLUSTER.
 FT METAL 26 26 CLUSTER.
 FT METAL 16 16 CLUSTER.
 FT METAL 18 18 CLUSTER.
 FT METAL 21 21 CLUSTER.
 SQ SEQUENCE 60 AA; 6017 MN; E877334264C424A CRC64;

Query Match 100.0%; Score 52; DB 13; Length 60;
 Best Local Similarity 20.0%; Pred. No. 91;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXXXCXXXXXXCXXXC 20
 DR EMBL; AJ001584; CAA09714.1; -.

Db 28 CKKSCCPCCPSGCTKCASGC 47

RESULT 15
 093609 PRELIMINARY; PRT; 60 AA.
 AC 093609;
 DT 01-NOV-1998 (T-EMBL;el. 08, created)
 DT 01-NOV-1998 (T-EMBL;el. 08, Last sequence update)
 DT 01-OCT-2000 (T-EMBL;el. 15, Last annotation update)
 DE METALLOTHIONEIN (MT).
 GN MT.
 OS Trematomus bernacchii.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
 OC Nototherinidae; Nototherinidae; Trematomus.
 OX NCBI_TaxID=40690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Carginale V., Capasso C., Scudiero R., Parisi E.;
 RT "Metallothionein in Antarctic organisms";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDJB databases.
 CC FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE
 TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
 GLUCOCORTICOIDS.
 CC EMBL; AJ011585; CAA09715.1; -.
 DR HSSP; P02402, 1DPS
 DR INTERPRO; IPR000006; -.
 DR INTERPRO; IPR003019; -.
 DR PFAM; PF00131; metalthio; 1.
 DR PRINTS; PR00860; MVERTEBRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation; zinc.
 FT METAL 23 23 CLUSTER.
 FT METAL 26 26 CLUSTER.
 FT METAL 15 16 CLUSTER.
 FT METAL 18 18 CLUSTER.
 FT METAL 21 21 CLUSTER.
 FT METAL 30 30 CLUSTER.
 SQ SEQUENCE 60 AA; 6018 MW; AC66F3015A2C4251 CRC64;

Query Match 100.0%; Score 52; DB 13; Length 60;
 Best Local Similarity 20.0%; Pred. No. 91;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXXCXXXCXXXC 20	28 CKKSCCPCCPSGCTKCASGC 47
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Search completed: March 1, 2001, 16:22:07
 Job time: 284 sec